

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Loetscher, Marcel
Moser, Bernhard
- (ii) TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 - (B) STREET: Two Militia Drive
 - (C) CITY: Lexington
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02173
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patent In Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brook Esq., David E.
 - (B) REGISTRATION NUMBER: 22,592
 - (C) REFERENCE/DOCKET NUMBER: TKI96-01
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 861-6240
 - (B) TELEFAX: (617) 861-9540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1670 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 69..1172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCAACCACAA GCACCAAAGC AGAGGGGCAG GCAGCACACC ACCCAGCAGC CAGAGCACCA	60
GCCCAGCC ATG GTC CTT GAG GTG AGT GAC CAC CAA GTG CTA AAT GAC GCC	110
Met Val Leu Glu Val Ser Asp His Gln Val Leu Asn Asp Ala	
1 5 10	

GAG Glu 15	GTT Val	GCC Ala	GCC Ala	CTC Leu	CTG Leu 20	GAG Glu	AAC Asn	TTC Phe	AGC Ser	TCT Ser 25	TCC Ser	TAT Tyr	GAC Asp	TAT Tyr	GGA Gly 30	158
GAA Glu	AAC Asn	GAG Glu	AGT Ser	GAC Asp 35	TCG Ser	TGC Cys	TGT Cys	ACC Thr	TCC Ser 40	CCG Pro	CCC Pro	TGC Cys	CCA Pro	CAG Gln 45	GAC Asp	206
TTC Phe	AGC Ser	CTG Leu	AAC Asn 50	TTC Phe	GAC Asp	CGG Arg	GCC Ala	TTC Phe 55	CTG Leu	CCA Pro	GCC Ala	CTC Leu	TAC Tyr 60	AGC Ser	CTC Leu	254
CTC Leu	TTT Phe	CTG Leu 65	CTG Leu	GGG Gly	CTG Leu	CTG Leu	GGC Gly 70	AAC Asn	GGC Gly	GCG Ala	GTG Val	GCA Ala 75	GCC Ala	GTG Val	CTG Leu	302
CTG Leu	AGC Ser 80	CGG Arg	CGG Arg	ACA Thr	GCC Ala	CTG Leu 85	AGC Ser	AGC Ser	ACC Thr	GAC Asp 90	ACC Thr	TTC Phe	CTG Leu	CTC Leu	CAC His	350
CTA Leu 95	GCT Ala	GTA Val	GCA Ala	GAC Asp	ACG Thr 100	CTG Leu	CTG Leu	GTG Val	CTG Leu	ACA Thr 105	CTG Leu	CCG Pro	CTC Leu	TGG Trp	GCA Ala 110	398
GTG Val	GAC Asp	GCT Ala	GCC Ala	GTC Val 115	CAG Gln	TGG Trp	GTC Val	TTT Phe	GGC Gly 120	TCT Ser	GGC Gly	CTC Leu	TGC Cys	AAA Lys 125	GTG Val	446
GCA Ala	GGT Gly	GCC Ala	CTC Leu 130	TTC Phe	AAC Asn	ATC Ile	AAC Asn	TTC Phe 135	TAC Tyr	GCA Ala	GGA Gly	GCC Ala	CTC Leu 140	CTG Leu	CTG Leu	494
GCC Ala	TGC Cys	ATC Ile 145	AGC Ser	TTT Phe	GAC Asp	CGC Arg	TAC Tyr 150	CTG Leu	AAC Asn	ATA Ile	GTT Val	CAT His 155	GCC Ala	ACC Thr	CAG Gln	542
CTC Leu 160	TAC Tyr	CGC Arg	CGG Arg	GGG Gly	CCC Pro	CCG Pro 165	GCC Ala	CGC Arg	GTG Val	ACC Thr 170	CTC Leu	ACC Thr	TGC Cys	CTG Leu	GCT Ala	590
GTC Val 175	TGG Trp	GGG Gly	CTC Leu	TGC Cys	CTG Leu 180	CTT Leu	TTC Phe	GCC Ala	CTC Leu	CCA Pro 185	GAC Asp	TTC Phe	ATC Ile	TTC Phe	CTG Leu 190	638
TCG Ser	GCC Ala	CAC His	CAC His	GAC Asp 195	GAG Glu	CGC Arg	CTC Leu	AAC Asn	GCC Ala 200	ACC Thr	CAC His	TGC Cys	CAA Gln	TAC Tyr 205	AAC Asn	686
TTC Phe	CCA Pro	CAG Gln 210	GTG Val	GGC Gly	CGC Arg	ACG Thr	GCT Ala	CTG Leu 215	CGG Arg	GTG Val	CTG Leu	CAG Gln	CTG Leu 220	GTG Val	GCT Ala	734
GGC Gly	TTT Phe	CTG Leu 225	CTG Leu	CCC Pro	CTG Leu	CTG Leu	GTC Val 230	ATG Met	GCC Ala	TAC Tyr	TGC Cys	TAT Tyr 235	GCC Ala	CAC His	ATC Ile	782
CTG Leu 240	GCC Ala	GTG Val	CTG Leu	CTG Leu	GTT Val	TCC Ser 245	AGG Arg	GGC Gly	CAG Gln	CGG Arg	CGC Arg	CTG Leu	CGG Arg	GCC Ala	ATG Met	830

CGG CTG GTG GTG GTG GTC GTG GTG GCC TTT GCC CTC TGC TGG ACC CCC	878
Arg Leu Val Val Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro	
255 260 265 270	
TAT CAC CTG GTG GTG CTG GTG GAC ATC CTC ATG GAC CTG GGC GCT TTG	926
Tyr His Leu Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu	
275 280 285	
GCC CGC AAC TGT GGC CGA GAA AGC AGG GTA GAC GTG GCC AAG TCG GTC	974
Ala Arg Asn Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val	
290 295 300	
ACC TCA GGC CTG GGC TAC ATG CAC TGC TGC CTC AAC CCG CTG CTC TAT	1022
Thr Ser Gly Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr	
305 310 315	
GCC TTT GTA GGG GTC AAG TTC CGG GAG CGG ATG TGG ATG CTG CTC TTG	1070
Ala Phe Val Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu	
320 325 330	
CGC CTG GGC TGC CCC AAC CAG AGA GGG CTC CAG AGG CAG CCA TCG TCT	1118
Arg Leu Gly Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser	
335 340 345 350	
TCC CGC CGG GAT TCA TCC TGG TCT GAG ACC TCA GAG GCC TCC TAC TCG	1166
Ser Arg Arg Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser	
355 360 365	
GGC TTG TGAGGCCGGA ATCCGGGCTC CCCTTTCGCC CACAGTCTGA CTTCCCCGCA	1222
Gly Leu	
TTCCAGGCTC CTCCCTCCCT CTGCCGGCTC TGGCTCTCCC CAATATCCTC GCTCCCGGGA	1282
CTCACTGGCA GCCCCAGCAC CACCAGGTCT CCCGGAAGC CACCCTCCCA GCTCTGAGGA	1342
CTGCACCATT GCTGCTCCTT AGCTGCCAAG CCCCATCCTG CCGCCCGAGG TGGCTGCCTG	1402
GAGCCCCACT GCCCTTCTCA TTTGGAACT AAAACTTCAT CTTCCCCAAG TGCGGGGAGT	1462
ACAAGGCATG GCGTAGAGGG TGCTGCCCCA TGAAGCCACA GCCCAGGCCT CCAGCTCAGC	1522
AGTGACTGTG GCCATGGTCC CCAAGACCTC TATATTGCT CTTTTATTTT TATGTCTAAA	1582
ATCCTGCTTA AAACCTTTTCA ATAAACAAGA TCGTCAGGAC CTTTTTTTTT TTTTTTTTTT	1642
TTTTTTTTTT TTTTTTTTTT TTTTTTTT	1670

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Val	Leu	Glu	Val 5	Ser	Asp	His	Gln	Val 10	Leu	Asn	Asp	Ala	Glu 15	Val
Ala	Ala	Leu	Leu 20	Glu	Asn	Phe	Ser	Ser 25	Ser	Tyr	Asp	Tyr	Gly 30	Glu	Asn
Glu	Ser	Asp 35	Ser	Cys	Cys	Thr	Ser 40	Pro	Pro	Cys	Pro	Gln 45	Asp	Phe	Ser
Leu	Asn 50	Phe	Asp	Arg	Ala	Phe 55	Leu	Pro	Ala	Leu	Tyr 60	Ser	Leu	Leu	Phe
Leu 65	Leu	Gly	Leu	Leu	Gly 70	Asn	Gly	Ala	Val	Ala 75	Ala	Val	Leu	Leu	Ser 80
Arg	Arg	Thr	Ala	Leu 85	Ser	Ser	Thr	Asp	Thr 90	Phe	Leu	Leu	His	Leu 95	Ala
Val	Ala	Asp	Thr 100	Leu	Leu	Val	Leu	Thr 105	Leu	Pro	Leu	Trp	Ala 110	Val	Asp
Ala	Ala	Val 115	Gln	Trp	Val	Phe	Gly 120	Ser	Gly	Leu	Cys	Lys 125	Val	Ala	Gly
Ala	Leu 130	Phe	Asn	Ile	Asn	Phe 135	Tyr	Ala	Gly	Ala	Leu 140	Leu	Leu	Ala	Cys
Ile 145	Ser	Phe	Asp	Arg	Tyr 150	Leu	Asn	Ile	Val	His 155	Ala	Thr	Gln	Leu	Tyr 160
Arg	Arg	Gly	Pro	Pro 165	Ala	Arg	Val	Thr	Leu 170	Thr	Cys	Leu	Ala	Val 175	Trp
Gly	Leu	Cys	Leu 180	Leu	Phe	Ala	Leu	Pro 185	Asp	Phe	Ile	Phe	Leu 190	Ser	Ala
His	His	Asp 195	Glu	Arg	Leu	Asn	Ala 200	Thr	His	Cys	Gln	Tyr 205	Asn	Phe	Pro
Gln	Val 210	Gly	Arg	Thr	Ala	Leu 215	Arg	Val	Leu	Gln	Leu 220	Val	Ala	Gly	Phe
Leu 225	Leu	Pro	Leu	Leu	Val 230	Met	Ala	Tyr	Cys	Tyr 235	Ala	His	Ile	Leu	Ala 240
Val	Leu	Leu	Val	Ser 245	Arg	Gly	Gln	Arg	Arg 250	Leu	Arg	Ala	Met	Arg 255	Leu
Val	Val	Val	Val 260	Val	Val	Ala	Phe	Ala 265	Leu	Cys	Trp	Thr	Pro 270	Tyr	His
Leu	Val	Val 275	Leu	Val	Asp	Ile	Leu 280	Met	Asp	Leu	Gly	Ala 285	Leu	Ala	Arg
Asn	Cys 290	Gly	Arg	Glu	Ser	Arg 295	Val	Asp	Val	Ala	Lys 300	Ser	Val	Thr	Ser
Gly 305	Leu	Gly	Tyr	Met	His 310	Cys	Cys	Leu	Asn	Pro 315	Leu	Leu	Tyr	Ala	Phe 320
Val	Gly	Val	Lys 325	Phe	Arg	Glu	Arg	Met	Trp 330	Met	Leu	Leu	Leu	Arg 335	Leu

Tyr S
365

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ix) FEATURE:

- (A) NAME/KEY: modified_base
(B) LOCATION: 11
(D) OTHER INFORMATION: /mod base= i

(ix) FEATURE:

- ```
(A) NAME/KEY: modified_base
(B) LOCATION: 12
(D) OTHER INFORMATION: /mod base= i
```

(ix) FEATURE:

- ```
(A) NAME/KEY: modified_base
(B) LOCATION: 23
(D) OTHER INFORMATION: /mod base= i
```

(ix) FEATURE:

- ```
(A) NAME/KEY: modified_base
(B) LOCATION: 26
(D) OTHER INFORMATION: /mod base= i
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGCTGCAGC NNTKKCMGAC MTNCTNYT

28

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ix) FEATURE:

- ```
(A) NAME/KEY: modified_base
(B) LOCATION: 10
(D) OTHER INFORMATION: /mod base= i
```

(ix) FEATURE:

- (A) NAME/KEY: modified_base
(B) LOCATION: 16
(D) OTHER INFORMATION: /mod base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGTCTAGAN GGGTTNANRC ARCWRYG

27